

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 26, 2001, 01:20:46 : Search time 1967.09 Seconds
(without alignments)
12888.354 Million cell updates/sec

Title: US-09-707-121-1
Perfect score: 2682
Sequence: 1 atgttccctcaaaagacgc.....tccatctcctcaataatga 2682

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
listing first 45 summaries

Database :

EST:*

1: gb_est1:*\n2: gb_est2:*\n3: gb_est3:*\n4: gb_est4:*\n5: gb_est5:*\n6: gb_est6:*\n7: gb_est7:*\n8: gb_est8:*\n9: gb_est9:*\n10: gb_est10:*\n11: gb_est11:*\n12: gb_est12:*\n13: gb_est13:*\n14: gb_est14:*\n15: gb_est15:*\n16: gb_est16:*\n17: gb_est17:*\n18: gb_est18:*\n19: gb_est19:*\n20: gb_est20:*\n21: gb_est21:*\n22: gb_est22:*\n23: gb_est23:*\n24: gb_est24:*\n25: gb_est25:*\n26: gb_est26:*\n27: gb_est27:*\n28: gb_est28:*\n29: gb_est29:*\n30: gb_est30:*\n31: gb_est31:*\n32: gb_est32:*\n33: gb_est33:*\n34: gb_est34:*\n35: gb_est35:*\n36: gb_est36:*\n37: gb_est37:*\n38: gb_est38:*\n39: gb_est39:*\n40: gb_est40:*\n41: gb_est41:*\n42: gb_est42:*\n43: gb_est43:*\n44: gb_est44:*\n45: gb_est45:*\n46: gb_est46:*\n47: gb_est47:*\n48: gb_est48:*\n49: gb_est49:*\n50: gb_est50:*\n51: gb_est51:*\n52: gb_est52:*\n53: gb_est53:*\n54: gb_est54:*\n55: gb_est55:*\n56: gb_est56:*\n57: gb_est57:*\n58: gb_est58:*\n59: gb_est59:*\n60: gb_est60:*\n61: gb_est61:*\n62: gb_est62:*\n63: gb_est63:*\n64: gb_est64:*\n65: gb_est65:*\n66: gb_est66:*\n67: gb_est67:*\n68: gb_est68:*\n69: gb_est69:*\n70: gb_est70:*\n71: gb_est71:*\n72: gb_est72:*\n73: gb_est73:*\n74: gb_est74:*\n75: gb_est75:*\n76: gb_est76:*\n77: gb_est77:*\n78: gb_est78:*\n79: gb_est79:*\n80: gb_est80:*\n81: gb_est81:*\n82: gb_est82:*\n83: gb_est83:*\n84: gb_est84:*\n85: gb_est85:*\n86: gb_est86:*\n87: gb_est87:*\n88: gb_est88:*\n89: gb_est89:*\n90: gb_est90:*\n91: gb_est91:*\n92: gb_est92:*\n93: gb_est93:*\n94: gb_est94:*\n95: gb_est95:*\n96: gb_est96:*\n97: gb_est97:*\n98: gb_est98:*\n99: gb_est99:*\n100: gb_est100:*\n101: gb_est101:*\n102: gb_est102:*\n103: gb_est103:*\n104: gb_est104:*\n105: gb_est105:*\n106: gb_est106:*\n107: gb_est107:*\n108: gb_est108:*\n109: gb_est109:*\n110: gb_est110:*\n111: gb_est111:*\n112: gb_est112:*\n113: gb_est113:*\n114: gb_est114:*\n115: gb_est115:*\n116: gb_est116:*

10267

44: em_esthum10:*\n45: em_esthum11:*\n46: em_esthum12:*\n47: em_esthum13:*\n48: em_esthum14:*\n49: em_esthum15:*\n50: em_esthum16:*\n51: em_esthum17:*\n52: em_esthum18:*\n53: em_esthum19:*\n54: em_esthum20:*\n55: em_esthum21:*\n56: em_esthum22:*\n57: em_esthum23:*\n58: em_esthum24:*\n59: em_esthum25:*\n60: em_esthum26:*\n61: em_esthum27:*\n62: em_esthum28:*\n63: em_esthum29:*\n64: em_esthum30:*\n65: em_esthum31:*\n66: em_esthum32:*\n67: em_esthum33:*\n68: em_esthum34:*\n69: em_esthum35:*\n70: em_esthum36:*\n71: em_esthum37:*\n72: em_esthum38:*\n73: em_esthum39:*\n74: em_esthum40:*\n75: em_esthum41:*\n76: em_esthum42:*\n77: em_esthum43:*\n78: em_esthum44:*\n79: em_esthum45:*\n80: em_esthum46:*\n81: em_esthum47:*\n82: em_esthum48:*\n83: em_esthum49:*\n84: em_esthum50:*\n85: em_esthum51:*\n86: em_esthum52:*\n87: em_esthum53:*\n88: em_esthum54:*\n89: em_esthum55:*\n90: em_esthum56:*\n91: em_esthum57:*\n92: em_esthum58:*\n93: em_esthum59:*\n94: em_esthum60:*\n95: em_esthum61:*\n96: em_esthum62:*\n97: em_esthum63:*\n98: em_esthum64:*\n99: em_esthum65:*\n100: em_esthum66:*\n101: em_esthum67:*\n102: em_esthum68:*\n103: em_esthum69:*\n104: em_esthum70:*\n105: em_esthum71:*\n106: em_esthum72:*\n107: em_esthum73:*\n108: em_esthum74:*\n109: em_esthum75:*\n110: em_esthum76:*\n111: em_esthum77:*\n112: em_esthum78:*\n113: em_esthum79:*\n114: em_esthum80:*\n115: em_esthum81:*\n116: em_esthum82:*

```

117: qb_cst148: *
118: qb_cst149: *
119: qb_cst150: *
120: qb_cst151: *
121: qb_cst152: *
122: qb_cst153: *
123: qb_cst154: *
124: qb_cst155: *
125: qb_cst156: *
126: qb_cst157: *
127: qb_cst158: *
128: qb_cst159: *
129: qb_cst160: *
130: qb_cst161: *
131: qb_cst162: *
132: qb_cst163: *
133: qb_cst164: *
134: qb_cst165: *
135: qb_cst166: *
136: qb_cst167: *
137: qb_cst168: *
138: qb_cst169: *
139: qb_cst170: *
140: qb_cst171: *
141: qb_cst172: *
142: qb_cst173: *
143: qb_cst174: *
144: qb_cst175: *
145: qb_cst176: *
146: qb_cst177: *
147: qb_cst178: *
148: qb_cst179: *
149: qb_cst180: *
150: qb_cst181: *
151: qb_cst182: *
152: qb_cst183: *
153: qb_cst184: *
154: qb_cst185: *
155: qb_cst186: *
156: qb_cst187: *
157: qb_cst188: *
158: qb_cst189: *
159: qb_cst190: *
160: qb_cst191: *
161: qb_cst192: *
162: qb_cst193: *
163: qb_cst194: *
164: qb_cst195: *
165: qb_cst196: *
166: qb_cst197: *
167: qb_cst198: *
168: qb_cst199: *
169: qb_cst200: *
170: qb_cst201: *
171: qb_cst202: *
172: qb_cst203: *
173: qb_cst204: *
174: qb_cst205: *
175: qb_cst206: *
176: qb_cst207: *
177: qb_cst208: *
178: qb_cst209: *
179: qb_cst210: *
180: qb_cst211: *
181: qb_cst212: *
182: qb_cst213: *
183: qb_cst214: *
184: qb_cst215: *
185: qb_cst216: *
186: qb_cst217: *
187: qb_cst218: *
188: qb_cst219: *
189: qb_cst220: *

```

```

190: qb_cst110: *
191: qb_cst111: *
192: qb_cst112: *
193: qb_cst113: *
194: qb_cst114: *
195: qb_cst115: *
196: qb_cst116: *
197: qb_cst117: *
198: qb_cst118: *
199: qb_cst119: *
200: qb_cst120: *
201: qb_cst121: *
202: qb_cst122: *
203: qb_cst123: *
204: qb_cst124: *
205: qb_cst125: *
206: qb_cst126: *
207: qb_cst127: *
208: qb_cst128: *
209: qb_cst129: *
210: qb_cst130: *
211: qb_cst131: *
212: qb_cst132: *
213: qb_cst133: *
214: qb_cst134: *
215: qb_cst135: *
216: qb_cst136: *
217: qb_cst137: *
218: qb_cst138: *
219: qb_cst139: *
220: qb_cst140: *
221: qb_cst141: *
222: qb_cst142: *
223: qb_cst143: *
224: qb_cst144: *
225: qb_cst145: *
226: qb_cst146: *
227: qb_cst147: *
228: qb_cst148: *
229: qb_cst149: *
230: qb_cst150: *
231: qb_cst151: *
232: qb_cst152: *
233: qb_cst153: *
234: qb_cst154: *
235: qb_cst155: *
236: qb_cst156: *
237: qb_cst157: *
238: qb_cst158: *
239: qb_cst159: *
240: qb_cst160: *
241: qb_cst161: *
242: qb_cst162: *
243: qb_cst163: *
244: qb_cst164: *
245: qb_cst165: *
246: qb_cst166: *
247: qb_cst167: *
248: qb_cst168: *
249: qb_cst169: *
250: qb_cst170: *
251: qb_cst171: *
252: qb_cst172: *
253: qb_cst173: *
254: qb_cst174: *
255: qb_cst175: *
256: qb_cst176: *
257: qb_cst177: *
258: qb_cst178: *

```

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

H84971
 LACTIS
 DEFINITION Y889d07.r1 Soares retina N2b5HR Homo sapiens cDNA clone
 IMAGE:221965 5', mRNA sequence.
 ACCESSION H84971
 VERSION H84971.1 GI:1064604
 SOURCE EST.
 ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 415)
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
 The WashU-Merck EST Project
 Unpublished (1995)
 JOURNAL Contact: Wilson RK
 COMMENT Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 High quality sequence stops: 311
 Source: IMAGE Consortium, LNL
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert length: 2075 Std Error: 0.00
 Seq primer: M13RP1
 High quality sequence stop: 311.
 Location/Qualifiers
 1..415
 /organism="Homo sapiens"
 /db_xref="GDB:3850726"
 /db_xref="taxon:9606"
 /clone="IMAGE:221965"
 /clone_1lb="Soares retina N2b5HR"
 /sex="male"
 /tissue_type="retina"
 /dev_stage="55 year old"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: eye; Vector: pTZ19 (Pharmacia) with a modified polylinker; Site: 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer 15' TGTACCAATCTGCAAGTGAAGCGGCGCCATTTTCTTTTCTTTT 3', double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTZ19 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)⁺ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Beato Soares and M. Fatima Bonaldo."

BASE COUNT 129 a 82 c 85 g 114 t 5 others
 ORIGIN
 Query Match 13.5%; Score 361.8; DB 158; Length 415;
 Best Local Similarity 98.4%; Pred. No. 1,3e-89;
 Matches 374; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
 Oy 1161 gctaaagaatgaatgaatgtttgtgtgtgaacattttaccaccatttgaagaaga 1220
 Db 11 gctaaagaatgaatgaatgtttgtgtgaacattttaccaccatttgaagaaga 70
 Oy 1221 ccaagctaaattactcctcaacaagaatgaatgttctgaagctgcacacgtcc 1280
 Db 71 ccaagctaaattactcctcaacaagaatgaatgttctgaagctgcacacgtcc 130
 Oy 1281 ttaactcaagaagaagaatgaatgaatgaatgaatgaatgaatgaatgaatga 1340
 Db 11 ttaactcaagaagaagaatgaatgaatgaatgaatgaatgaatgaatgaatga 11

Db 131 TTTATCATCGAGAGAGAGATACAGATACCAACTAAATGATTTCTTCGACAG 190
 Oy 1341 gctgctaaagcttaccatataaaacacacacacacacacacacacacacacac 1400
 Db 191 gctgctaaagcttaccatataaaacacacacacacacacacacacacacacac 250
 Oy 1401 tccctcctatagaaagaaatgaagaaatgaagaaatgaagaaatgaagaaatga 1460
 Db 251 tccctcctatagaaagaaatgaagaaatgaagaaatgaagaaatgaagaaatga 310
 Oy 1461 tgcacagtaacagtaacagtaacagtaacagtaacagtaacagtaacagtaac 1519
 Db 311 tgcacagtaacagtaacagtaacagtaacagtaacagtaacagtaacagtaac 370
 Oy 1520 tgcacagtaacagtaacagtaacagtaacagtaacagtaacagtaacagtaac 1539
 Db 371 tgcacagtaacagtaacagtaacagtaacagtaacagtaacagtaacagtaac 390

RESULT 14
 LOCUS N50504 514 bp mRNA EST 14-FEB-1996
 DEFINITION Y889d07.r1 Soares multiple_sclerosis_2N0HNSP Homo sapiens cDNA
 clone IMAGE:280659 5', mRNA sequence.
 ACCESSION N50504
 VERSION N50504.1 GI:1191670
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 514)
 AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.
 The WashU-Merck EST Project
 Unpublished (1995)
 JOURNAL Contact: Wilson RK
 COMMENT Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 High quality sequence stops: 335.
 Source: IMAGE Consortium (info@image.lnl.gov) for further information.
 Seq primer: 77
 High quality sequence stop: 335.
 Location/Qualifiers
 1..514
 /organism="Homo sapiens"
 /db_xref="GDB:3899035"
 /db_xref="taxon:9606"
 /clone="IMAGE:280659"
 /clone_1lb="Soares multiple_sclerosis_2N0HNSP"
 /sex="male"
 /tissue_type="multiple sclerosis lesions"
 /dev_stage="Age 46"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Vector: pTZ19 (Pharmacia) with a modified polylinker V-TYPE; phagemid: Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer 15' TGTACCAATCTGCAAGTGAAGCGGCGCCATTTTCTTTTCTTTT 3', double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTZ19 vector (Pharmacia). Library went through one round of normalization to a Cot - 5, library constructed by Beato Soares and M. Fatima Bonaldo. RNA from 4 multiple sclerosis lesions from one patient was kindly provided by Dr. Kevin G. Becker (NINDS/NIH)."

BASE COUNT 148 a 123 c 114 g 120 t 9 others

Db 525 GAAATATCCAGAGGTCTGCATTCTAGATGGGGGATTACAGATCAGGCCAACAGGCT 584
Uy 2655 cctcaccatcccatctctcctcaaatatga 2682
||||| ||| ||||||| |||||
Db 585 CCTCAGGCTCCCTCTCTCTCAGATATGA 612

Search completed: June 26, 2001, 01:58:17
Job time: 2251 sec

FRAGMENT TYPE: N-terminal
US-08-894-274-10

Query Match 5.6%; Score 265; DB 2; Length 326;
Best Local Similarity 29.0%; Pred. No. 3,2e-18;
Matches 94; Conservative 49; Mismatches 97; Indels 84; Gaps 16;

```

QY 25 GSNGLPTPNISKILGRVLIKTHPRICQYD---ISRKHE-RLVVAHECHERLED 80
DB 50 GEEGMPL--STIREVAVKHLETFEHPVAVVRLDVCIVSRDRKTKLTVFENXQDLTT 107
QY 81 LLREKRP---VSCSTVLCIAEVLQYMKHGIHRAISPHNILLDRKHILAKFGL 137
DB 108 YL-DKVEPGVPTETIKMKMQLLGLDLSHHVYHDKPKQNLIVTSSQIKLADFG 166
QY 148 YHMTAHGSDVDFPIGYS-----YLAPEVIAQGIPTTDMPSKKPLSPSPKDWASIG 191
DB 167 ARI-----YSFOMALTSVVVTLWYRAPEVLLQSSVAT-----PV-----DLMSVG 206
QY 192 ILLEFLCVRKLFQ-SLUISEKFLILLDCVDDTLIVLAHEHGLD1----- 238
DB 207 CIFAEPMFRKRLFGSSSDVDLQKIL-----DIVIGLGEEDMPRDVALPRQAFHSKSA 259
QY 239 -----IKELPEYVIDLANKCLTFHPSKRPDPDELMKDKVSEVSPLYTPPTKPSLFS 292
DB 260 QPIEFVVDIDELGKLLKCLTFNPAKR-----ISAYSALSHPY-----FQD 302
QY 293 SLRC---ADILTPEDISQICKDIN 313
DB 303 LERCKENLDSHLP--SONTSELN 324

```

RESULT 4

```

US-08-581-918A-10
: Sequence 10, Application US/08581918A
: Patent No. 6043030
: GENERAL INFORMATION:
: APPLICANT: Beach, David H.
: APPLICANT: Demetrick, Douglas J.
: APPLICANT: Serrano, Manuel
: TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
: TITLE OF INVENTION: Related Thereto
: NUMBER OF SEQUENCES: 49
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Foley, Hoag & Eliot
: STREET: One Post Office Square
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Wordpad
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/581,918A
: FILING DATE: 02-JAN-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/497,214
: FILING DATE: 30-JUN-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/446,147
: FILING DATE: 29-NOV-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/306,511
: FILING DATE: 14-SEP-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/248,812
: FILING DATE: 25-MAY-1994

```

```

: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/227,371
: FILING DATE: 14-Apr-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/154,915
: FILING DATE: 18-NOV-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/991,997
: FILING DATE: 17-DEC-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Vincent, Matthew P.
: REGISTRATION NUMBER: 36,709
: REFERENCE/DOCKET NUMBER: MIV-071,06
: TELEPHONE: (617) 832-7000
: TELEFAX: (617) 832-7000
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 326 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: Protein
: FRAGMENT TYPE: N-terminal
US-08-581-918A-10

```

Query Match 5.4%; Score 253; DB 3; Length 326;
Best Local Similarity 28.7%; Pred. No. 5.3e-17;
Matches 93; Conservative 48; Mismatches 99; Indels 84; Gaps 16;

```

QY 25 GSNGLPTPNISKILGRVLIKTHPRICQYD---ISRKHE-RLVVAHECHERLED 80
DB 50 GEEGMPL--STIREVAVKHLETFEHPVAVVRLDVCIVSRDRKTKLTVFENXQDLTT 107
QY 81 LLREKRP---VSCSTVLCIAEVLQYMKHGIHRAISPHNILLDRKHILAKFGL 137
DB 108 YL-DKVEPGVPTETIKMKMQLLGLDLSHHVYHDKPKQNLIVTSSQIKLADFG 166
QY 138 YHMTAHGSDVDFPIGYS-----YLAPEVIAQGIPTTDMPSKKPLSPSPKDWASIG 191
DB 167 ARI-----YSFOMALTSVVVTLWYRAPEVLLQSSVAT-----PV-----DLMSVG 206
QY 192 ILLEFLCVRKLFQ-SLUISEKFLILLDCVDDTLIVLAHEHGLD1----- 238
DB 207 CIFAEPMFRKRLFGSSSDVDLQKIL-----DIVIGLGEEDMPRDVALPRQAFHSKSA 259
QY 239 -----IKELPEYVIDLANKCLTFHPSKRPDPDELMKDKVSEVSPLYTPPTKPSLFS 292
DB 260 QPIEFVVDIDELGKLLKCLTFNPAKR-----ISAYSALSHPY-----FQD 302
QY 293 SLRC---ADILTPEDISQICKDIN 313
DB 303 LERCKENLDSHLP--SONTSELN 324

```

RESULT 5

```

US-08-346-147B-10
: Sequence 10, Application US/08346147B
: Patent No. 6211334
: GENERAL INFORMATION:
: APPLICANT: Beach, David H.
: APPLICANT: Demetrick, Douglas J.
: APPLICANT: Serrano, Manuel
: TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
: TITLE OF INVENTION: Related Thereto
: NUMBER OF SEQUENCES: 47
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Foley, Hoag & Eliot
: STREET: One Post Office Square
: CITY: Boston
: STATE: MA
: COUNTRY: USA

```

```

2 ZIP: 02109
3 COMPUTER READABLE FORM:
4 MEDIUM TYPE: floppy disk
5 COMPUTER: IBM pc compatible
6 OPERATING SYSTEM: pc dos/ms dos
7 SOFTWARE: Wordpad
8 CURRENT APPLICATION DATA:
9 APPLICATION NUMBER: US/08/146, 147B
10 FILING DATE: 29 Nov 1994
11 CLASSIFICATION: 514
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: US 08/406, 511
14 FILING DATE: 14 SEP 1994
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: US 08/248, 812
17 FILING DATE: 25 MAY 1994
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: US 08/227, 471
20 FILING DATE: 14 Apr 1994
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: US 08/154, 915
23 FILING DATE: 18 Nov 1994
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 02/991, 997
26 FILING DATE: 17 DEC 1992
27 ATTORNEY/AGENT INFORMATION:
28 NAME: Vincent, Matthew P.
29 REGISTRATION NUMBER: 46, 709
30 REFERENCE/PACKET NUMBER: MIV 071, 04
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: (617) 832 1299
33 TELEFAX: (617) 832 7000
34 INFORMATION FOR SEQ ID NO: 10:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 426 amino acids
37 TYPE: amino acid
38 TOPOLOGY: linear
39 MOLECULE TYPE: protein
40 FRAGMENT TYPE: N-terminal
41 US 08 822 936 10

```

```

Query Match 5.4K; Score 293; DB 4; Length 426;
Post Local Similarity 28.7K; Pred. No. 5, 6-17;
Matches 94; Conservative 48; Mismatches 99; Indels 84; Gaps 16;

25 GSNGLPLPNSIKLIGFGLKTTTHPRGCGYVD ISKSKHE KLVVVAEHCERSLEP 80
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
50 GEDRPL STTRVAVAKHLETFEIRNVVAFPLVTSSTDFEKLIVPEXXVQULTT 107
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
81 LLEERKP VSTSTVLTAPEVAGLQYNNKRGIVHVALSPINILAEKCHIKAKGL 147
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
108 YLDRVPEVGFETIKIMPFQGLDGLDPLSHVNVVHRODKIPNLTVTSSQIKLADGG 166
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
138 YHMTARHDEVEPTGYPS YLAPEVLAQTEKFTDHMSKRLDPSGRPSWSLQ 191
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
167 ARI YSFQALISVVVTLWYRAIVGLSSVAL IV-----DLSWVG 206
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
192 LLEFDVAKRFG SDLSIRAKGLTLTLCVVDITLVLAPEHCITL----- 248
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
207 CTFAEERPRKIDFGSSSVQGLKTL IVTGLPDEHMDIPIVALLRQVAFHSSKA 259
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
239 -----KRLPEVTLIDNKLTLFHSKRPDPDELAKDKVFSVSPLYTPTKVASLSS 292
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
260 QPTEKVIDHDEGRDLKTLFENAKK ISAVSALSHRY-----FQD 302
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
293 SLGK--ADLLIDEDLSQIKDIN 314
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
303 LERKKNLSHIPP--SNTSTSLN 324
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

```

RESULT 6
US 08 822 936 10

```

2 Sequence 10, Application US/08822936
3 Patent No. 6,242,575
4 GENERAL INFORMATION:
5 APPLICANT: Massano, Joan
6 APPLICANT: Roberts, James M.
7 APPLICANT: Kott, Andrew
8 APPLICANT: Kolyak, Kordelia
9 TITLE OF INVENTION: Isolated p27 protein, Nucleic Acid
10 TITLE OF INVENTION: Molecules Encoding Same, Methods of Identifying Agents Acti
11 TITLE OF INVENTION: and Uses of Said Agents
12 NUMBER OF SEQUENCES: 10
13 CORRESPONDENT ADDRESS:
14 ADDRESSEE: Policy, Road & Fleet, LLP
15 STREET: One Post Office Square
16 CITY: Boston
17 STATE: MA
18 COUNTRY: USA
19 ZIP: 02109-2170
20 COMPUTER READABLE FORM:
21 MEDIUM TYPE: floppy disk
22 COMPUTER: IBM pc compatible
23 OPERATING SYSTEM: pc dos/ms dos
24 SOFTWARE: Patent In Release #1.0, Version #1.25
25 CURRENT APPLICATION DATA:
26 APPLICATION NUMBER: US/08/822, 936
27 FILING DATE: 21 FEBRUARY 1997
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Vincent, Matthew P.
30 REGISTRATION NUMBER: 46, 709
31 REFERENCE/PACKET NUMBER: MIV-079, 05
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (617) 832-1000
34 TELEFAX: (617) 832 7000
35 INFORMATION FOR SEQ ID NO: 10:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 426 amino acids
38 TYPE: amino acid
39 TOPOLOGY: linear
40 MOLECULE TYPE: protein
41 FRAGMENT TYPE: N-terminal
42 US 08 822 936-10

```

```

Query Match 5.4K; Score 254; DB 4; Length 426;
Post Local Similarity 28.7K; Pred. No. 5, 6-17;
Matches 94; Conservative 48; Mismatches 99; Indels 84; Gaps 16;

25 GSNGLPLPNSIKLIGFGLKTTTHPRGCGYVD ISKSKHE KLVVVAEHCERSLEP 80
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
50 GEDRPL STTRVAVAKHLETFEIRNVVAFPLVTSSTDFEKLIVPEXXVQULTT 107
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
81 LLEERKP VSTSTVLTAPEVAGLQYNNKRGIVHVALSPINILAEKCHIKAKGL 147
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
108 YLDRVPEVGFETIKIMPFQGLDGLDPLSHVNVVHRODKIPNLTVTSSQIKLADGG 166
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
138 YHMTARHDEVEPTGYPS YLAPEVLAQTEKFTDHMSKRLDPSGRPSWSLQ 191
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
167 ARI YSFQALISVVVTLWYRAIVGLSSVAL IV-----DLSWVG 206
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
192 LLEFDVAKRFG SDLSIRAKGLTLTLCVVDITLVLAPEHCITL----- 248
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
207 CTFAEERPRKIDFGSSSVQGLKTL IVTGLPDEHMDIPIVALLRQVAFHSSKA 259
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
239 -----KRLPEVTLIDNKLTLFHSKRPDPDELAKDKVFSVSPLYTPTKVASLSS 292
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
260 QPTEKVIDHDEGRDLKTLFENAKK ISAVSALSHRY-----FQD 302
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
293 SLGK--ADLLIDEDLSQIKDIN 314
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
303 LERKKNLSHIPP--SNTSTSLN 324
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

```

RESULT 7

Query Match 5.08; Score 235; DB 2; Length 372;
 Best Local Similarity 24.5%; Pred. No. 4.5e-15;
 Matches 94; Conservative 62; Mismatches 145; Indels 82; Gaps 16;

```

QY 3 PLEKEMGAFTFPASALPDVWG-----SNGPLTPNSIKIGRPQILKTTTPRLCO 55
DB 34 PIKPIGRKAVGTCSSVNNETNEKAIAKKINNAFENRIDALRTLRKILRLRHEENVIA 93
QY 56 VYUHSRGRH-----LVVAEHGENSELDELREKRVSCSTVLCIAFVYLGLOVMKNG 111
DB 94 LKIVMPPHRSRPFKYIAYELMDITLHOIKSSQTLSDHCQYFELFOLLRLCKYLSAN 153
QY 112 IVHKAISPNILLDKRGHAKFGLYHMTANGDDVDFICGPPS---YIAPFVIAQGLFK 168
DB 154 ILHRDILKPGNLLINANCOKICDFGLAR-TSSGKO-QEPFVYVTRWYRAPELL----- 206
QY 169 TTHHMSKKPLSPGSPKSWSLGIIIFELCVGRK-LFOSLDSIRLKLTL-LDCVDPDL 226
DB 207 CCDDN-----GTSIDWMSVGCIFAEI-LGRKVFPTGTCINOLKILINLGSOREO 257
QY 227 IVLAHEGGLDILKELPET-----VILNKLGLTFHPSKRPDPDELMDK 271
DB 258 IEFIDPKARKYIKSLPSPGTPSRILYPHAPLAIDLQRMVLPDPSSKRSIVIALQHP 317
QY 272 VSEVSPLYTPTFKPASILPSSSLRCADLLTPEDISQCKDINNYLAESILEVYIWLCT 331
DB 318 Y---MSPLIDPNTDPAQVYINL-----DDED-LGBTIREM--MW-- 353
QY 332 AGGDELEKELVNEKILRSKPIC 354
DB 354 -----SPILEYHPEAF 365

```

RESULT 15
 US-09-031-563-7
 : Sequence 7, Application US/09031563A
 : Patent No. 6022708
 : GENERAL INFORMATION:
 : APPLICANT: Frederic de Sauvage
 : APPLICANT: Atrion Roshenthal
 : TITLE OF INVENTION: Fused
 : FILE REFERENCE: P1272
 : CURRENT APPLICATION NUMBER: US/09/031,563A
 : CURRENT FILING DATE: 1998-02-26
 : NUMBER OF SEQ ID NOS: 27
 : SEQ ID NO 7
 : LENGTH: 647
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 : US-09-031-563-7

Query Match 4.9%; Score 231.5; DB 3; Length 647;
 Best Local Similarity 22.0%; Pred. No. 2.8e-14;
 Matches 136; Conservative 82; Mismatches 202; Indels 197; Gaps 27;

```

QY 43 QILKTTTPRLCOYVDISGRGHERLVVAEHGENSELDELREKRVSCSTVLCIAFVLO 102
DB 53 EIMKGRHRIHVMILD-SFTDKEVVYVDYVAEGHFOILEDGKLPEDOVOAIAQVLS 111
QY 103 GLOVMKNGHIVHKAISPNILLDKRGHAKFGLYHMTANGDDVDFI-GYPSYLAPEV 161
DB 112 ALYLLSHRIHMDKPFUNLLAKGGITKLCDFGARASTNTMTVITSIKGIPYMSPEL 171
QY 162 IAGGIFKTTDHMSKKPLSPGSPKSWSLGIIIFELCVGRKLFOSLDSIRLKLTLDC 221
DB 172 VER--RPYDH-----FADLMSVGCILYLAAGTPPPYATSIQVLSLIK---- 214
QY 222 VDTITVLAHEGGLDILKELPETV---DLNKLGLTFHPSKRPDPDELMDKVESFV 276
DB 215 -----DPVR-WPSTISPCPKNFLOGILTKDPRQLSWPDLVHPFIAGHV 258

```

```

QY 277 S-----PLYTPFKPASILPSSSLRCADLLTPEDISQCKD-----IN 314
DB 259 TITTEPAPDLGTPPTS-----RLPEEL-QVTKDQAHRLAKGNOSHL 304
QY 314 NDY--IAERSIEVYVLMCLAGDLEKIVNKEIIRKSPICLPNPLFEDGSPGCGRD 371
DB 304 QAYKMAFEAMOKHO---NTGPALDEDEKTSKVAQIAPLPRL-----CATPQ 349
QY 372 RSSLDDITVTLSLCOLNRRLKDWGEAPPLHDDQSNIPHSNNPLSAAATPLIR 431
DB 350 ESSLGAGI-----IASLKL-----SSWAKSGTGEVPSAPR 379
QY 432 EKDTEYQINRIILFBRILKAFYKKNOIWKREAPDIFPLMK-----GITWALIGVCAI 486
DB 380 ENRTTPDGER-----AFEPERPEVLGGRSTIDVDLENEPPDSNFWOHL----- 424
QY 487 HAKYDAIDKTPDIPTDROLEVDIHCHOYDEILSSPEQ-----HAKFRVILKAV-- 546
DB 425 -----FTTPVP---IQIKAPL-----TLGCPNPPCGORTOSQIHFAAGQILKGLIG 468
QY 537 VSH--PDIYVWQGLDSICAPPLVYLFNNEALVACMSAFTIKYL----- 578
DB 469 ASHILPAFRVLSLISGSS-----DSVALYSYCKEAGILPGLLSLRHSQESNSLQOQ 521
QY 579 --YNFELKDNSHVTOEY 593
DB 522 SWYGTFLQDLMAVIOAY 538

```

Search completed: August 12, 2002, 09:04:24
 Job time: 3811 sec

•
•

Genforce version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: June 26, 2001, 01:21:46 ; Search time 3505.23 Seconds
(without alignments)
11835.030 Million cell updates/sec

Title: US-09-707-121-1

Perfect score:

2682

Sequence: 1 atgttccctcaaaacacg.....tccatctcctcaaatatga 2682

Scoring table:

IDENTITY MUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 773874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

(GenEmbl):
1: gb_ba1:*
2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
5: gb_in2:*
6: gb_in3:*
7: gb_om:*
8: gb_ov:*
9: gb_pat1:*
10: gb_pat2:*
11: gb_ph:*
12: gb_pl1:*
13: gb_pl2:*
14: gb_pl3:*
15: gb_pl4:*
16: em_ba1:*
17: em_ba2:*
18: em_ino:*
19: em_hao_hum:*
20: em_hao_inv:*
21: em_hao_rod:*
22: em_htg_hum1:*
23: em_htg_hum2:*
24: em_htg_hum3:*
25: em_htg_hum4:*
26: em_htg_hum5:*
27: em_htg_hum6:*
28: em_htg_hum7:*
29: em_htg_hum8:*
30: em_htg_inv1:*
31: em_htg_inv2:*
32: em_htg_other:*
33: em_htg_rod:*
34: em_hum1:*
35: em_hum2:*
36: em_hum3:*
37: em_hum4:*
38: em_hum5:*
39: em_hum6:*
40: em_hum7:*
41: em_in:*
42: em_om:*
43: em_or:*

44: em_ov:*
45: em_pat:*
46: em_ph:*
47: em_pl:*
48: em_ro:*
49: em_sus:*
50: em_sy:*
51: em_un:*
52: em_v1:*
53: gb_srs1:*
54: gb_srs2:*
55: gb_srs3:*
56: gb_sy:*
57: gb_un:*
58: gb_v12:*
59: gb_v12:*
60: gb_hq1:*
61: gb_hq2:*
62: gb_hq3:*
63: gb_hq4:*
64: gb_hq5:*
65: gb_hq6:*
66: gb_hq7:*
67: gb_hq8:*
68: gb_hq9:*
69: gb_hq10:*
70: gb_hq11:*
71: gb_hq12:*
72: gb_hq13:*
73: gb_hq14:*
74: gb_hq15:*
75: gb_hq16:*
76: gb_hq17:*
77: gb_hq18:*
78: gb_hq19:*
79: gb_hq20:*
80: gb_hq21:*
81: gb_hq22:*
82: gb_hq23:*
83: gb_hq24:*
84: gb_hq25:*
85: gb_pr1:*
86: gb_pr2:*
87: gb_pr3:*
88: gb_pr4:*
89: gb_pr5:*
90: gb_pr6:*
91: gb_pr7:*
92: gb_pr8:*
93: gb_pr9:*
94: gb_pr10:*
95: gb_pr11:*
96: gb_pr12:*
97: gb_pr13:*
98: em_ba3:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query length	DB ID	Description
1	2659.6	99.2	2679	10	AX099148
2	1463.4	54.6	2428	89	AF161420
3	193	7.2	99878	77	AC087108
4	193	7.2	116822	83	AP002076
5	179.2	6.7	116530	83	AP001957
6	178.6	6.7	116530	83	AP001957
7	178.6	6.7	135584	66	AC020749
8	169.8	6.3	135584	66	AC020749


```
QY 2012 taactaatgctttaaataatatactctctctctcgaattacagaataattgaatctg 2071
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 40085 tcaacttccggtttcaacacagtcgaacgcttctctctctcgaaccccatatccgtaggg 40144
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2072 aacgtctgtgtgagagaactcttaacctgtttctgttgacttcttaaaatgctacttaca 2131
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 40145 atgactgtgtgtctgagtcacacagagatgtatcaggaagccacacagagagattattactcattc 40204
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 2132 gacagcatgctcaacctccaaagcc 2156
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 40205 gccagctaccccttgcgccctccatgcc 40229
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

Search completed: June 26, 2001, 03:16:41
Job time: 6905 sec


```

Db 329 TAEELKCKFFK-----AKNREYLIEKL-----LITPDLAQRKRVKRVGSSGHL 376
Cc 318 AENSIEFEVYIACGLDLEKELVKNKILRSKPICTILNLFEDGK-SPGQGRDSSILA 376
Cc 377 --HKTRGQDMFWS-----DDEMFGRS-----FKCAASQSKSRVKE 412
Cc 377 DDTVTLSLQLENRKDKVGEAFYPLEDDQSNLPHSNNSNELSAATLPLIRKQTE 436
Cc 413 ENPEIASASTIPEQIUS-----LSVHDSQSPNANRKYRASSCAVNLVILKNSR 464
Cc 437 YQUNRI-----ILF-----DRLKATPYKKNOIWKARADIPPLMR 472
Cc 465 KELNDIEFEETPGEDTADGVSELEFSAGLVGDHYIVANLQK-----IVDDPKALK 517
Cc 473 GLFWALLGVGGA 485
Cc 518 TLTPKIASGDCDS 530

RESULT 9
K110_ARA1H STANDARD: PRT: 512 AA.
AC 038997: Q39076: Q04728:
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE SNF1-RELATED PROTEIN KINASE KIN10 (EC 2.7.1.-) (AKIN10).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; Eudicotyledons; core eudicot; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN 111
RP SEQUENCE FROM N.A.
RX MEDLINE=93013041; PubMed=1339373;
RA Le Guen L., Thomas M., Bianchi M., Hallard N.G., Kreis M.;
RT Structure and expression of a gene from Arabidopsis thaliana
RT encoding a protein related to SNF1 protein kinase.*;
RI Gene 120:249-254(1992).
RN 121
RP SEQUENCE FROM N.A.
RX STRAIN=CV, COLOMBIA;
RA Lessard P., Kreis M.;
RI Submitted (JBC-1996) to the EMBL/GenBank/DBJ databases.
RN 131
RP SEQUENCE FROM N.A.
RX STRAIN=CV, COLOMBIA;
RA Lin X., Kaul S., Town C.D., Benito M., Greasy T.H., Haas B., Wu D.,
RA Rongman C.M., Koo H., Fujii C.Y., Ditzelback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Niernm W.G., Fraser C.M.;
RI Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN 141
RP SEQUENCE OF 1-19 FROM N.A.
RX STRAIN=CV, COLOMBIA;
RA MEDLINE=95115691; PubMed=7816049;
RA Le Guen L., Thomas M., Kreis M.;
RI "Gene density and organization in a small region of the Arabidopsis
RI thaliana genome.*";
RL Mol. Gen. Genet. 245:390-396(1994).
Cc 1-1 FUNCTION: MAY PLAY AN IMPORTANT ROLE IN A SIGNAL TRANSDUCTION
Cc CASCADE REGULATING GENE EXPRESSION AND CARBOHYDRATE METABOLISM IN
Cc HIGHER PLANTS.
Cc 1-1 TISSUE SPECIFICITY: EXPRESSED IN ROOTS, SHOOTS AND LEAVES.
Cc 1-1 SIMILARITY: BELONGS TO THE SHK/THK FAMILY OF PROTEIN KINASES.
Cc SNF1 SUBFAMILY.
Cc 1-1 This SWISS-PROT entry is copyright. It is produced through a collaboration
Cc between the Swiss Institute of Bioinformatics and the EMBL outstation -
Cc the European Bioinformatics Institute. There are no restrictions on its
Cc use by non-profit institutions as long as its content is in no way
Cc modified and this statement is not removed. Usage by and for commercial
Cc entities requires a license agreement (see http://www.isb-sib.ch/announce/)

```

```

Cc or send an email to license@sib.ch).
Cc EMBL: M93023; AAA32736.1;
Cc DR EMBL: X79707; CAA56146.1;
Cc DR EMBL: AC008261; AAF20165.1;
Cc DR EMBL: X94757; CAA64384.1;
Cc DR Mendel: 14016; ARALh:2326; m14016.
Cc DR Mendel: 12898; ARALh:2098.1.
Cc DR InterPro: IPR000449;
Cc DR InterPro: IPR000719;
Cc DR InterPro: IPR001245;
Cc DR InterPro: IPR002290;
Cc DR Pfam: PF00627; UBA: 1.
Cc DR Pfam: PF00069; pkinase: 1.
Cc DR PRINTS: PR00109; TYRKINASE.
Cc DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
Cc DR PROSITE: PS50011; PROTEIN_KINASE_SF_1.
Cc DR Transferrase: Serine/threonine-protein kinase; ATP-binding;
Cc KW Phosphorylation.
Cc FT DOMAIN 19 271 PROTEIN KINASE.
Cc FT NP_BIND 25 33 ATP (BY SIMILARITY).
Cc FT BINDING 48 48 ATP (BY SIMILARITY).
Cc FT ACT_SITE 142 142 BY SIMILARITY.
Cc FT MOD_RES 175 175 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
Cc SQ SEQUENCE 512 AA: 58373 MW: 5A18655A0AA506DE CRC64:

Query Match 5.3%; Score 252; Dn 1; length 512;
Best Local Similarity 22.0%; Pred. No. 2.2e-09;
Matches 85; Conservative 59; Mismatches 129; Indels 114; Gaps 7;

Cc 35 SIKLQK-----FOILKTTTHPIQGVYDLSKSKHRIVVAHCRSLF 79
Cc 46 AILKLNRRKIKNMEMREKREIKILRLPMHPTIKLFEVILPTVIVMEYVNSGELP 105
Cc 80 DLREKRPVSGSTVLCIAEVLQGYMNKRGIVRALSPHNLDRKSHIKLAKGLYH 139
Cc 106 DYIVGKRIQEDHARRNPGQILISGVYCHNNVYHRLKPNILLSKCNVKRAIDGSLN 165
Cc 140 MIAHGDVDPFICYPSTLADPVAAGCFKTTDMSKPLPSQKSDVNSIGILFEICV 199
Cc 166 IMRDGHEFKTSGSPYVAPEVINGKLY-----ASPEVDVNSGVILVALLG 212
Cc 200 GRKLPQSLDSHKIKLTLDCVDITLVIARHSGCIDLKELEPVILNKLTFHPS 259
Cc 213 GTLPEDDENIPNLFKRI-----KCGIYTLPSHSISPGAKDIPPMIAVDPM 257
Cc 260 KRPTPELMKDKVESEVSPLYTFPTKPAISLFSSSLRCADLTLPEDISQCKOINDYLAE 319
Cc 258 KAVTIPETRIQHMPVQAHLPYLAVP-----PPDIYQQAKKIKDELTL-- 298
Cc 320 RSLIEVYIIMGLACGLDLEKELVKNKILRSKPICTILNLFEDGKSPGQGRDSSILA 379
Cc 299 -----DEVIN-----MGFDRNHLIE-- 313
Cc 380 VTTLSLQLENRKDKVGEAFYPLEDD 406
Cc 314 -----SLNRTQNDGVIVYVILIDN 313

RESULT 10
Cc5_YEAST STANDARD: PRT: 705 AA.
AC P32362;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CELL CYCLE PROTEIN KINASE CDC5/MSD2 (EC 2.7.1.-)
Cc CDC5 OR PKX2 OR MSD2 OR YMR001C OR YMR270.03C.
Cc OS Saccharomyces cerevisiae (Baker's yeast).
Cc Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Cc Saccharomycetales; Saccharomycetaceae; Saccharomyces.

```



```

CC BECOME EXOCRINE EXPRESSED IN CHOROID PLEXUS DEVELOPING;
CC
CC -1- REMAIN: PAPA BOX (PROLINE-ALANINE REPEATS) MAY TARGET THE KINASE
CC TO A SPECIFIC SUBCELLULAR LOCATION BY FACILITATING INTERACTION
CC WITH INTRACELLULAR PROTEINS SUCH AS ACTIN OR ACTIN-LIKE PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC STE20 SUBFAMILY.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: D88190; HAA26000.1;
CC EMBL: AF068261; AAC23501.1;
CC EMBL: AF099990; AAC72239.1;
CC HSSP: P00518; 1PKK.
CC InterPro: IPR000719;
CC Pfam: PF00069; Kinase; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00107; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC Transferrase: Serine/threonine-protein kinase; ATP-binding.
CC
CC DOMAIN 14 62
CC NE_BIND 72 346 PROTEIN KINASE.
CC BINDING 78 86 ATP (BY SIMILARITY).
CC ACT_SITE 101 101 ATP (BY SIMILARITY).
CC ACT_SITE 201 201 BY SIMILARITY.
CC DOMAIN 22 30 POLY-ALA.
CC SITE 369 475 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC SITE 396 400 CASPASE CLEAVAGE RELATED SITE.
CC CONFLICT 11 11 V -> I (IN REF. 2).
CC CONFLICT 253 253 M -> I (IN REF. 2).
CC CONFLICT 403 403 E -> Q (IN REF. 2).
CC SEQUENCE 553 AA: 60050 MW: 86C1458AEAF690C8 CRC64;

```

Query Match: 5.3%; Score 250; DB 1; Length 553;
 Best Local Similarity: 23.9%; Pred. No. 3.3e-09;
 Matches 118; Conservative 81; Mismatches 179; Indels 116; Gaps 20;

```

QY 37 KILASFOILKTIHPRLCYVDYISGKHRLVVAHCEGERSLEHLR-----ERK-pv 88
DB 114 ELKRLQMSQSHNNVYTYTSYVAKDRLMVMKLLSGSMILIKTVKRGKHKVYL 173
QY 89 SCSTVLCIAFEVLOGLOYNKRHGVHRALESPHILLDRKGHIKLAEGVYHMTAGDDVD 148
DB 174 EEAIIATILKLEVLISGLDYLHNGOIHRLKAGNILLGEGSVQIADFGVSAMIAIGDVT 233
QY 149 FP-----IGPSYIAPRYVIAQGIPTKTDHMDSKKPLPSGKRSYWSIGIILFELCVGRK 202
DB 244 RNKYKRTVGVPCWMAPEVMEQ--VRGYDF-----KADWMSGIIATIELATGAA 280
QY 203 LPSQIDISERIKPLTIDCVDDITVLAEEHOGCLDIKELEPVIDLKNKIFPHSKRP 262
DB 281 PYHKYPPKAVL--MLTIONPPPLFTGVGRK--FMKKYKTSKPKLLSLICKQDPKRP 335
QY 263 TPDELAKDVESEVSPLYPTKPAFLSSSSLRKADLTLPEDISOLCKDI-----NDYL 317
DB 346 TAAELIKCKPFQK-----AKNNEYIIEKI-----LTKPTDIAQRAKKYKRVHSSGHL 383
QY 318 AKRSIHEVYIIMQLAGCLKEKLVNKKIIRSKPPLCTLPNLFEDGSGPFGGGRDSSLLD 377
DB 384 --HKTEDDWMS-----DDEMEKRS-----EGKA--AASQESKREVK 418
QY 378 DTTVITISGLKRLKLVGCG--EAFYPLEDDQSNIPHSNNSNLSAATPLPLIIRKDT 435
DB 419 KENPPISTV-----NAGCIPTFOIGLSVHDSQOPANEDYRIGRCPA--VNIIVIRLINS 469
QY 436 EYOLNRI-----ILF-----DRLKAYPYKKNOIMKEARVDIPELM 471

```

```

DB 470 RKEINDIREFTPGRTADGVSELFSAGLVADIDVIVANLQK-----YDDPKAL 522
QY 472 KGLTWMALGVGCA 485
DB 523 KILFKLASGIDGA 536

```

RESULT 12
 PLOT_SCHPO
 ID PLOT_SCHPO STANDARD; PRT: 683 AA.
 AC P50528;
 DT 01-OCT-1996 (Rel. 34, created)
 DT 01-OCT-1996 (Rel. 34, last sequence update)
 DT 01-OCT-2000 (Rel. 40, last annotation update)
 DE SRINE/THREONINE-PROTEIN KINASE PLOT (EC 2.7.1.-).
 GN PLOT OR SPAC23C11.16.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OX NCBI_TaxID:4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RX MEDLINE-95262899; PubMed-7744248;
 RA Okura H., Hagan J.M., Glover J.M.;
 RT "The conserved Schizosaccharomyces pombe kinase PLOT, required to
 RT form a bipolar spindle, the actin ring, and septum, can drive septum
 RT formation in G1 and G2 cells.";
 RT Genes Dev. 9:1059-1073(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RA Brown D., Churcher C.M., Bartell H.G., Kaandream M.A., Wood V.;
 RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: REQUIRED TO FORM A BIPOLAR SPINDLE, THE ACTIN RING AND
 CC SEPTUM. FUNCTIONS UPSTREAM OF THE WHOLE SEPTUM FORMATION PATHWAY,
 CC INCLUDING ACTIN RING FORMATION (REGULATED BY LATE SEPTATION GENES)
 CC AND SEPTAL MATERIAL DEPOSITION (REGULATED BY EARLY SEPTATION
 CC GENES). BEHAVES AS A "SEPTUM-PROMOTING FACTOR", AND COULD ALSO BE
 CC INVOLVED IN INDUCING OTHER LATE EVENTS OF CELL DIVISION.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CDC5/POLO SUBFAMILY.
 CC
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: X85758; CAA59766.1;
 CC EMBL: Z98559; CAB1167.1;
 CC HSSP: Q63450; 1A06.
 CC InterPro: IPR000719;
 CC InterPro: IPR000959;
 CC InterPro: IPR002290;
 CC Pfam: PF00659; PLOT_Box; 2.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
 CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 CC Transferrase: Serine/threonine-protein kinase; ATP-binding.
 CC
 CC DOMAIN 41 296 PROTEIN KINASE.
 CC NE_BIND 47 55 ATP (BY SIMILARITY).
 CC BINDING 69 69 ATP (BY SIMILARITY).
 CC ACT_SITE 163 163 BY SIMILARITY.
 CC DOMAIN 493 522 POLO-HOMOLOGY (PH2).
 CC SEQUENCE 683 AA: 77301 MW: F1CD0EP9H913917 CRC64.

QY 140 MFAIRHIVITPTVPSYLAPEVIAAGLEKTTDIMPSSKRLPSGKSNVWSLGLLEFLAV 199
 DB 181 VMIDHILKISGSPSPYSGPVVSKLY 227
 QY 200 GRLKESLIDSESLKPELILAEVHDLVLAEHKKLIDLEKPEVYLINLKLTPPS 259
 DB 228 GILPILQDHLIPILKIL 300
 QY 240 KQPTPDELKQKVPSEVSPVYTPPEIKPASELSSSLKADLITPDISQLAKDINNOYLAE 319
 DB 273 KILITLQDHLIPILKIL 310
 QY 420 KSTEEVYTLKLADELKELVANKELLSKVPITTLNLEFEGES 373
 DB 411 GSKVKSIL 364
 QY 474 SLIDITVTLISLQULRNKIKOVCHAEVPLLEHQSNNLPSNSNNELSAATLILIRK 433
 DB 405 MESSLSPTLPSPT 419
 QY 444 LITVQLNRIILPEHLLKAVYKKNQIKKFAVNDLPIMLKILMA 491
 DB 420 MLC 463
 QY 492 ALUKITLPT 545
 DB 464 L SAPIVDTLQDKLILIKLQYKTRD 509
 QY 546 GELISLAPPL 556
 DB 510 LIL 517
 RESULT 5
 AA00416
 ID AA00416 standard; Protein: 509 AA
 AC AA00416
 XX
 DB 03 JAN 2001 (first entry)
 DE Corn putative carbon catabolite repression protein SNF #2.
 KW Corn carbon catabolite repression; sucrose non fermenting protein 1;
 KM SNF2; plant growth.
 OS Zea mays.
 FN W0200066115 A2.
 DB 22 JUN 2000.
 XX
 DE 15 DEC 1999; 99W0 US29824.
 XX
 DE 16 DEC 1998; 9808 0112563.
 XX
 DE (DDBP) J DBT ENT DE MEMBERS & CO E.L.
 XX
 DE Allen SM, Heppard EP, Sakai H, Wong Z, Helentjaris TG, Marcello DJ,
 PT Miao G.
 DB WPI: 2000 44596/37.
 DE N PS006 AAV52766.
 XX
 DE New nucleic acids encoding sucrose non fermenting 1 (SNF1) proteins
 PT involved in carbon catabolite repression in plants and seeds, useful
 PT for controlling carbon and nitrogen partitioning pathways during plant
 PT growth and development
 XX
 DE claim 10; page 45 46; 5pp; English.
 XX
 DE The present sequence is a putative sucrose non fermenting protein SNF1
 CC protein sequence from corn. Its coding sequence was isolated by searching

CC a corn casset shoot cDNA library for sequences similar to those encoding
 CC SNF1 in Arabidopsis thaliana, Oenothera sativa, glycine max and oryza
 CC sativa. The protein is involved in carbon catabolite repression, and so
 CC the gene and protein can be used in plants to control the nitrogen and
 CC carbon partitioning pathways during plant growth and development. They
 CC can also be used to alter the accumulation of carbohydrates, lipids and
 CC proteins during plant growth.
 XX
 SO Sequence 509 AA
 Query Match
 Best Local Similarity 22.7%; Score 264.5; EB 21; Length 509;
 Matches 114; Conservative 72; Mismatches 185; Indels 14; Gaps 16;
 QY 42 FOLIKITLIRKIDQYVDSISGKHEKRLVYVNGE--KSIPEHLEKRRKVSSTVLCAPV 100
 DB 66 LKILKILILPHILITLYEVYLPIDLYVMEYCKYQELIDYLOKRIQEDQARTILPIL 124
 QY 101 LQGLQYMKHIGIVHAKLSPINLLDKKGIKAKPOLYIMTANGIDVDEPGVSYLAPE 160
 DB 125 LSGVYCHRMVYHVDLKPILLDSKYVKKLADFGLSHMDGHLIKISGSPYGAAP 184
 QY 161 VINAQIFKTTDIMPSSKRLPSGKSNVWSLGLLEFLAVKRIKESLISEKILITLD 220
 DB 185 VLSKLY 227
 QY 221 GVDNLLVLAHEGCLDILKEPEVYDLNKLCPHPSKRPDDEMKIKVSESPY 280
 DB 228 281 TPTKPAFLSSSLKCAULTLPEDISQKIDINNDYLAERSIEEYVYLMVLAAGLEKEL 340
 DB 277 LAYP 299
 QY 341 VNKEILSKSPITLPLNLEFEGESFGSIRDSILIDITVTLSTQLNRKIKVGEAF 400
 DB 300 VMQTL 441
 QY 401 YPLEHQSNNLPSNSNNELSAATLILIRKIDVYLNKILPEHLLKAVYKKNQIKW 460
 DB 342 ADYQESMDRLNQIASSSSSLNYPQSAPL 389
 QY 461 KEARVNDLPIMLKILMAILGVEGALHAKYDAILKUTPITPDQIFVDIPKHYTELSS 520
 DB 390 521 SPEHAKFRRLKAWVSHPOL 542
 QY 419 KQNH 418
 RESULT 6
 AA055928
 ID AA055928 standard; Protein: 516 AA
 AC AA055928
 XX
 DE 18 FEB 2000 (first entry)
 DE Human STIK3 protein.
 XX
 DE Antithrombotic; anti-infective; anti-inflammatory; antiallergic; osteopathic;
 KW antipsoriatic; antiarthrosclerotic; antiasthmatic; immunosuppressive;
 KW neutroprotective; cardiatic; cerebroprotective; cytostatic; antiadhesive;
 KW vulnery; STE20; protein kinase; STIK2; STIK3; STIK4; STIK5; STIK6; STIK7;
 KW ZC1; ZC2; ZC3; ZC4; KHS2; STIK1; STIK4; GSK2; PAK4; PAK5; antagonistic;
 KW antibody gene therapy; rheumatoid arthritis; arteriosclerosis; asthma;
 KW inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
 KW thymus; autoimmunity; organ transplantation; multiple sclerosis;
 KW myocardial infarction; cardiovascular disease; stroke; renal failure;
 KW oxidative stress-related neurodegenerative disorder; Parkinson's disease;
 KW amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;
 KW

is ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis; mesangial disorder; growth regulation; wound healing; T cell activation; immunosuppressant.

Homo sapiens.

MO9953036-A2.

21-OCT-1999.

13-APR-1999: 99WO-0508150.

14-APR-1998: 98US-0081784.

(SUGEN) SUGEN INC.

Plowman G, Martinez R, Whyte D:

WPI: 1999-611301/52.

N-PSDB: AAZ40480.

Novel kinase-related polypeptides used for the diagnosis and treatment of kinase-related diseases and disorders.

Claim 11; page 260-262; 387pp; English.

This sequence represents a novel STE20-related protein kinase. The invention relates to nucleic acid molecule encoding a kinase polypeptide selected from STLK2, STLK3, STLK4, STLK5, STLK6, STLK7, ZC1, ZC2, ZC3, ZC4, KHS2, SUIJ1, SUIJ3, GSK2, PAK4 and PAK5. The proteins are used to identify agonists and antagonists, and to raise antibodies. The polynucleotides are useful in gene therapy protocols. The polynucleotides, polypeptides, antibodies, antagonists and agonists may be used to treat diseases such as immune-related disorders and diseases (e.g. rheumatoid arthritis, atherosclerosis, chronic inflammatory bowel disease (e.g. Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis, rheinits, autoimmunity, and organ transplantation, chronic inflammatory pelvic disease, multiple sclerosis, organ transplantation, myocardial infarction, cardiovascular disease, stroke, renal failure, oxidative stress-related neurodegenerative disorders (e.g. amyotrophic lateral sclerosis, Parkinson's disease and Leigh syndrome), cancer, cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes mellitus, fibrotic and mesangial disorders. The proteins may also be useful for cell growth regulation (e.g. in wound healing), T cell activation, mitosis control, and as immunosuppressants.

Sequence 516 AA:

Query Match 5.58; Score 260.5; DH 20; length 516;
Best Local Similarity 23.38; Pred. No. 1,le-15;
Matches 115; Conservative 86; Mismatches 179; Indels 113; Gaps 18;

37 KILGKQQLKLTTHPRICQYVDISCKGKHKLVVAHCKSKSLDLIR-----PKK--PV 88
Db 61 kllgkqmsqspnvvtysfvcakelwlmkllsqamldlkyivmggkngyl 135
QY 89 SCSTVLCIAFEVLGLOVMNKGIVHRLSPHINILLDRKKHILKAKRELIMYTAGDQVD 148
Db 146 ceatlatlkevgldythrngqthrdikagndllqcdgsqgladfgvsflatgavdt 195
QY 149 FPE-----IGVSYLAPVIAAGCIKLTIDHMSKKPLPSGKSDVWSGCIILFELCVGRK 202
Db 146 rnkvtklvqpcwapevmeq--vrygdi-----kadmwsldlaiaelaadaa 242
QY 203 LFOSLDISRLAKLTLDCCVDHLLVAEEHOCLODIKELEPVTVIDLAKCITPHPSKRP 262
Db 243 pyhkyppmkvll--mltlqdpfcltgyedk---cmnkkkygskfklstclqgdkpskrp 297
QY 263 TPDELMKQKVESEVSLPTFTKPSLFSSSLRCADLLPEDISQLCKDI-----NNYL 317
Db 298 taacellkckltfqq-----aknreyllekl-----lrcpldaqrakvtrvpgsqhl 345

QY 318 AEKSIPEVYVWCIACQDLKKEHVNKEHINSKPPICTLIPNLFEDCH-SKGQGRDSSIL 376
Db 346 --fkledqadews-----ddmdaks-----eekkaatsgsksrivke 381
QY 377 DDTVTLSLQLRNRLKDVGEAFYPLEDDQSNLPHSNNSNLSAATPLILIREKDE 446
Db 382 cnpelavsaastlpeqigs-----lsvhdsqgppanodyroascavnlvirftrsr 443
QY 437 YOLNRI-----ILF-----DRLLKAYFYKKNQJMKREARVDIPLMR 472
Db 434 kelndirfelftpardadvsqellsaqldqandvivaanlk-----lvdpbkak 466
QY 473 GILMAALLGVHCA 485
Db 487 llltklasqcdqs 499

RESULT 7
AAV01496
1D AAV01496 standard; peptide; 520 AA.

XX AC AAV01496;

XX XX 21-MAY-1999 (first entry)

XX DE Human pan-s/tk-1A receptor polypeptide.

XX KW Pancreatic serine/threonine kinase receptor; pan-s/tk; cell growth;
KW differentiation; gene therapy; ligand; screening; cell proliferation;
KW regulator; pancreatic.

XX OS Homo sapiens.

XX FI Key Location/Qualifiers

FT Misc-difference 11 /note="unspecified"

XX XX WO9907854-A2.

XX XX 18-FEB-1999.

XX XX 11-AUG-1998: 98WO-US16640.

XX XX 11-AUG-1997: 97US-0909354.

XX XX (ONTO-) ONTOGENY INC.

XX P1 Barker DD, Miao N, Pang K;

XX XX WPI: 1999-167430/14.

XX XX N-PSDB: AAX26148.

XX PT New pancreatic serine/threonine kinase (pan-s/tk) receptor
XX PT polypeptides - useful for modulating cell proliferation,
XX PS differentiation and survival in animals

PS Claim 1; page 66-67; 77pp; English.

The invention relates to isolated and/or recombinant pancreatic serine/threonine kinase receptor (pan-s/tk) polypeptides. Sequences of rat and human pan-s/tk polypeptides and nucleic acids encoding them are provided. Host cells containing recombinant vectors comprising the pan-s/tk genes are used for the recombinant expression of the proteins. The pan-s/tk polypeptides are useful for modulating cell growth, differentiation or survival in an animal cell. The polynucleotides are also useful for detecting pan-s/tk ligand on cells in samples and for gene therapy. Ligands identified, together with soluble polypeptides, are useful for screening test compounds that modulate the bioactivity of a pan-s/tk receptor. The discovery of this new class of pan-s/tk polypeptides provides an alternative method of mediating cell proliferation, differentiation and survival in animals. The polypeptides also represent the first identified specific regulators of pancreatic development. The present sequence represents a human pan-s/tk-1A receptor polypeptide.

AG6157;
XX 18-JUN-2000 (first entry)
XX Arabidopsis thaliana protein fragment SpQ ID NO: 44272.
XX Protein identification: signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX Arabidopsis thaliana.
XX EPI034405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000RP-0301434.
XX 25-FEB-1999; 9905-0121825.
XX 05-MAR-1999; 9905-0123180.
XX 09-MAR-1999; 9905-0123548.
XX 23-MAR-1999; 9905-0125788.
XX 25-MAR-1999; 9905-0126264.
XX 29-MAR-1999; 9905-0126785.
XX 01-APR-1999; 9905-0127462.
XX 06-APR-1999; 9905-0128234.
XX 08-APR-1999; 9905-0128714.
XX 16-APR-1999; 9905-0129845.
XX 19-APR-1999; 9905-0130077.
XX 21-APR-1999; 9905-0130449.
XX 23-APR-1999; 9905-0130510.
XX 23-APR-1999; 9905-0130891.
XX 28-APR-1999; 9905-0131449.
XX 30-APR-1999; 9905-0132048.
XX 30-APR-1999; 9905-0132407.
XX 04-MAY-1999; 9905-0132484.
XX 05-MAY-1999; 9905-0132485.
XX 06-MAY-1999; 9905-0132486.
XX 06-MAY-1999; 9905-0132487.
XX 07-MAY-1999; 9905-0132863.
XX 11-MAY-1999; 9905-0134256.
XX 14-MAY-1999; 9905-0134218.
XX 14-MAY-1999; 9905-0134219.
XX 14-MAY-1999; 9905-0134221.
XX 14-MAY-1999; 9905-0134370.
XX 18-MAY-1999; 9905-0134768.
XX 19-MAY-1999; 9905-0134941.
XX 20-MAY-1999; 9905-0135124.
XX 21-MAY-1999; 9905-0135351.
XX 24-MAY-1999; 9905-0135629.
XX 25-MAY-1999; 9905-0136021.
XX 27-MAY-1999; 9905-0136392.
XX 28-MAY-1999; 9905-0136782.
XX 01-JUN-1999; 9905-0137222.
XX 03-JUN-1999; 9905-0137528.
XX 04-JUN-1999; 9905-0137502.
XX 07-JUN-1999; 9905-0137724.
XX 08-JUN-1999; 9905-0138094.
XX 10-JUN-1999; 9905-0138540.
XX 14-JUN-1999; 9905-0138847.
XX 14-JUN-1999; 9905-0139119.
XX 16-JUN-1999; 9905-0139452.
XX 16-JUN-1999; 9905-0139453.
XX 17-JUN-1999; 9905-0139492.
XX 18-JUN-1999; 9905-0139454.
XX 18-JUN-1999; 9905-0139455.
XX 18-JUN-1999; 9905-0139456.
XX 18-JUN-1999; 9905-0139457.
XX 18-JUN-1999; 9905-0139458.
XX 18-JUN-1999; 9905-0139459.
XX 18-JUN-1999; 9905-0139460.
XX 18-JUN-1999; 9905-0139461.
XX 18-JUN-1999; 9905-0139462.

PR 18-JUN-1999; 9905-0139463.
PR 18-JUN-1999; 9905-0139750.
PR 18-JUN-1999; 9905-0139763.
PR 21-JUN-1999; 9905-0139817.
PR 22-JUN-1999; 9905-0139899.
PR 23-JUN-1999; 9905-0140353.
PR 23-JUN-1999; 9905-0140354.
PR 24-JUN-1999; 9905-0140695.
PR 28-JUN-1999; 9905-0140823.
PR 29-JUN-1999; 9905-0140991.
PR 30-JUN-1999; 9905-0141287.
PR 01-JUL-1999; 9905-0141842.
PR 01-JUL-1999; 9905-0142154.
PR 02-JUL-1999; 9905-0142055.
PR 06-JUL-1999; 9905-0142390.
PR 08-JUL-1999; 9905-0142803.
PR 09-JUL-1999; 9905-0142920.
PR 12-JUL-1999; 9905-0142977.
PR 13-JUL-1999; 9905-0143542.
PR 14-JUL-1999; 9905-0143624.
PR 15-JUL-1999; 9905-0144005.
PR 16-JUL-1999; 9905-0144085.
PR 16-JUL-1999; 9905-0144086.
PR 19-JUL-1999; 9905-0144325.
PR 19-JUL-1999; 9905-0144331.
PR 19-JUL-1999; 9905-0144332.
PR 19-JUL-1999; 9905-0144333.
PR 19-JUL-1999; 9905-0144334.
PR 20-JUL-1999; 9905-0144335.
PR 20-JUL-1999; 9905-0144352.
PR 20-JUL-1999; 9905-0144632.
PR 20-JUL-1999; 9905-0144684.
PR 21-JUL-1999; 9905-0144814.
PR 21-JUL-1999; 9905-0145086.
PR 21-JUL-1999; 9905-0145088.
PR 22-JUL-1999; 9905-0145085.
PR 22-JUL-1999; 9905-0145087.
PR 22-JUL-1999; 9905-0145089.
PR 22-JUL-1999; 9905-0145192.
PR 23-JUL-1999; 9905-0145145.
PR 23-JUL-1999; 9905-0145218.
PR 23-JUL-1999; 9905-0145224.
PR 26-JUL-1999; 9905-0145276.
PR 27-JUL-1999; 9905-0145913.
PR 27-JUL-1999; 9905-0145918.
PR 27-JUL-1999; 9905-0145919.
PR 28-JUL-1999; 9905-0145951.
PR 02-AUG-1999; 9905-0146386.
PR 02-AUG-1999; 9905-0146388.
PR 02-AUG-1999; 9905-0146389.
PR 03-AUG-1999; 9905-0147038.
PR 04-AUG-1999; 9905-0147204.
PR 04-AUG-1999; 9905-0147302.
PR 05-AUG-1999; 9905-0147192.
PR 05-AUG-1999; 9905-0147260.
PR 06-AUG-1999; 9905-0147303.
PR 06-AUG-1999; 9905-0147416.
PR 06-AUG-1999; 9905-0147417.
PR 09-AUG-1999; 9905-0147493.
PR 09-AUG-1999; 9905-0147935.
PR 10-AUG-1999; 9905-0148171.
PR 11-AUG-1999; 9905-0148319.
PR 12-AUG-1999; 9905-0148341.
PR 13-AUG-1999; 9905-0148565.
PR 13-AUG-1999; 9905-0148684.
PR 16-AUG-1999; 9905-0149368.
PR 17-AUG-1999; 9905-0149175.
PR 18-AUG-1999; 9905-0149426.
PR 20-AUG-1999; 9905-0149722.
PR 20-AUG-1999; 9905-0149723.
PR 20-AUG-1999; 9905-0149929.
PR 23-AUG-1999; 9905-0149902.
PR 23-AUG-1999; 9905-0149930.
PR 25-AUG-1999; 9905-0150566.

PR 14 MAY-1999; 9905-0143370.
PR 18 MAY-1999; 9905-0143768.
PR 19 MAY-1999; 9905-0143941.
PR 20 MAY-1999; 9905-0145124.
PR 21 MAY-1999; 9905-0135353.
PR 24 MAY-1999; 9905-0135629.
PR 25 MAY-1999; 9905-0136021.
PR 27 MAY-1999; 9905-0136302.
PR 28 MAY-1999; 9905-0136782.
PR 01 JUN-1999; 9905-0137222.
PR 03 JUN-1999; 9905-0137528.
PR 04 JUN-1999; 9905-0137502.
PR 07 JUN-1999; 9905-0137724.
PR 08 JUN-1999; 9905-0138004.
PR 10 JUN-1999; 9905-0138540.
PR 14 JUN-1999; 9905-0138847.
PR 16 JUN-1999; 9905-0139119.
PR 16 JUN-1999; 9905-0139452.
PR 16 JUN-1999; 9905-0139453.
PR 17 JUN-1999; 9905-0139492.
PR 18 JUN-1999; 9905-0139454.
PR 18 JUN-1999; 9905-0139455.
PR 18 JUN-1999; 9905-0139456.
PR 18 JUN-1999; 9905-0139457.
PR 18 JUN-1999; 9905-0139458.
PR 18 JUN-1999; 9905-0139459.
PR 18 JUN-1999; 9905-0139460.
PR 18 JUN-1999; 9905-0139461.
PR 18 JUN-1999; 9905-0139462.
PR 18 JUN-1999; 9905-0139463.
PR 18 JUN-1999; 9905-0139750.
PR 18 JUN-1999; 9905-0139763.
PR 21 JUN-1999; 9905-0139817.
PR 22 JUN-1999; 9905-0139899.
PR 23 JUN-1999; 9905-0140354.
PR 23 JUN-1999; 9905-0140354.
PR 24 JUN-1999; 9905-0140695.
PR 28 JUN-1999; 9905-0140823.
PR 29 JUN-1999; 9905-0140991.
PR 30 JUN-1999; 9905-0141287.
PR 01 JUL-1999; 9905-0141842.
PR 01 JUL-1999; 9905-0142154.
PR 02 JUL-1999; 9905-0142055.
PR 06 JUL-1999; 9905-0142390.
PR 08 JUL-1999; 9905-0142803.
PR 09 JUL-1999; 9905-0142920.
PR 12 JUL-1999; 9905-0142977.
PR 13 JUL-1999; 9905-0143542.
PR 14 JUL-1999; 9905-0143624.
PR 15 JUL-1999; 9905-0144005.
PR 16 JUL-1999; 9905-0144085.
PR 16 JUL-1999; 9905-0144086.
PR 19 JUL-1999; 9905-0144325.
PR 19 JUL-1999; 9905-0144331.
PR 19 JUL-1999; 9905-0144332.
PR 19 JUL-1999; 9905-0144333.
PR 19 JUL-1999; 9905-0144334.
PR 19 JUL-1999; 9905-0144335.
PR 20 JUL-1999; 9905-0144352.
PR 20 JUL-1999; 9905-0144632.
PR 20 JUL-1999; 9905-0144684.
PR 21 JUL-1999; 9905-0144814.
PR 21 JUL-1999; 9905-0145086.
PR 21 JUL-1999; 9905-0145088.
PR 22 JUL-1999; 9905-0145087.
PR 22 JUL-1999; 9905-0145088.
PR 22 JUL-1999; 9905-0145192.
PR 23 JUL-1999; 9905-0145145.
PR 23 JUL-1999; 9905-0145218.
PR 23 JUL-1999; 9905-0145224.
PR 26 JUL-1999; 9905-0145276.
PR 27 JUL-1999; 9905-0145913.

PR 27 JUL-1999; 9905-0145918.
PR 27 JUL-1999; 9905-0145919.
PR 28 JUL-1999; 9905-0145951.
PR 02 AUG-1999; 9905-0146385.
PR 02 AUG-1999; 9905-0146386.
PR 02 AUG-1999; 9905-0146387.
PR 03 AUG-1999; 9905-0146389.
PR 04 AUG-1999; 9905-0147038.
PR 04 AUG-1999; 9905-0147038.
PR 05 AUG-1999; 9905-0147302.
PR 05 AUG-1999; 9905-0147192.
PR 05 AUG-1999; 9905-0147260.
PR 06 AUG-1999; 9905-0147303.
PR 06 AUG-1999; 9905-0147416.
PR 09 AUG-1999; 9905-0147493.
PR 09 AUG-1999; 9905-0147935.
PR 10 AUG-1999; 9905-0148171.
PR 11 AUG-1999; 9905-0148319.
PR 12 AUG-1999; 9905-0148341.
PR 13 AUG-1999; 9905-0148565.
PR 13 AUG-1999; 9905-0148684.
PR 16 AUG-1999; 9905-0149368.
PR 17 AUG-1999; 9905-0149175.
PR 18 AUG-1999; 9905-0149426.
PR 20 AUG-1999; 9905-0149722.
PR 20 AUG-1999; 9905-0149723.
PR 20 AUG-1999; 9905-0149929.
PR 23 AUG-1999; 9905-0149902.
PR 23 AUG-1999; 9905-0149930.
PR 25 AUG-1999; 9905-0150566.
PR 26 AUG-1999; 9905-0150884.
PR 27 AUG-1999; 9905-0151065.
PR 27 AUG-1999; 9905-0151066.
PR 27 AUG-1999; 9905-0151080.
PR 30 AUG-1999; 9905-0151303.
PR 31 AUG-1999; 9905-0151438.
PR 01 SEP-1999; 9905-0151930.
PR 07 SEP-1999; 9905-0152363.
PR 10 SEP-1999; 9905-0153070.
PR 13 SEP-1999; 9905-0153758.
PR 15 SEP-1999; 9905-0154018.
PR 16 SEP-1999; 9905-0154039.
PR 20 SEP-1999; 9905-0154079.
PR 22 SEP-1999; 9905-0155139.
PR 23 SEP-1999; 9905-0155486.
PR 24 SEP-1999; 9905-0155659.
PR 28 SEP-1999; 9905-0156458.
PR 29 SEP-1999; 9905-0156596.
PR 04 OCT-1999; 9905-0157117.
PR 05 OCT-1999; 9905-0157753.
PR 06 OCT-1999; 9905-0157865.
PR 07 OCT-1999; 9905-0158029.
PR 08 OCT-1999; 9905-0158232.
PR 12 OCT-1999; 9905-0158369.
PR 13 OCT-1999; 9905-0159293.
PR 13 OCT-1999; 9905-0159294.
PR 13 OCT-1999; 9905-0159295.
PR 14 OCT-1999; 9905-0159329.
PR 14 OCT-1999; 9905-0159330.
PR 14 OCT-1999; 9905-0159331.
PR 14 OCT-1999; 9905-0159637.
PR 14 OCT-1999; 9905-0159638.
PR 18 OCT-1999; 9905-0159584.
PR 21 OCT-1999; 9905-0160741.
PR 21 OCT-1999; 9905-0160767.
PR 21 OCT-1999; 9905-0160768.
PR 21 OCT-1999; 9905-0160770.
PR 21 OCT-1999; 9905-0160814.
PR 21 OCT-1999; 9905-0160815.
PR 22 OCT-1999; 9905-0160980.
PR 22 OCT-1999; 9905-0160981.
PR 22 OCT-1999; 9905-0160989.
PR 25 OCT-1999; 9905-0161404.
PR 25 OCT-1999; 9905-0161405.


```

PR 08-JUL-1999: 990S-0142803.
PR 09-JUL-1999: 990S-0142920.
PR 12-JUL-1999: 990S-0142977.
PR 13-JUL-1999: 990S-0143542.
PR 14-JUL-1999: 990S-0143624.
PR 15-JUL-1999: 990S-0144005.
PR 16-JUL-1999: 990S-0144085.
PR 16-JUL-1999: 990S-0144086.
PR 19-JUL-1999: 990S-0144325.
PR 19-JUL-1999: 990S-0144331.
PR 19-JUL-1999: 990S-0144332.
PR 19-JUL-1999: 990S-0144333.
PR 19-JUL-1999: 990S-0144334.
PR 19-JUL-1999: 990S-0144335.
PR 20-JUL-1999: 990S-0144352.
PR 20-JUL-1999: 990S-0144632.
PR 21-JUL-1999: 990S-0144684.
PR 21-JUL-1999: 990S-0144814.
PR 21-JUL-1999: 990S-0145086.
PR 21-JUL-1999: 990S-0145088.
PR 22-JUL-1999: 990S-0145085.
PR 22-JUL-1999: 990S-0145087.
PR 22-JUL-1999: 990S-0145089.
PR 22-JUL-1999: 990S-0145192.
PR 23-JUL-1999: 990S-0145145.
PR 23-JUL-1999: 990S-0145218.
PR 23-JUL-1999: 990S-0145224.
PR 26-JUL-1999: 990S-0145276.
PR 27-JUL-1999: 990S-0145913.
PR 27-JUL-1999: 990S-0145918.
PR 27-JUL-1999: 990S-0145919.
PR 28-JUL-1999: 990S-0145951.
PR 02-AUG-1999: 990S-0146386.
PR 02-AUG-1999: 990S-0146388.
PR 02-AUG-1999: 990S-0146389.
PR 03-AUG-1999: 990S-0147038.
PR 04-AUG-1999: 990S-0147204.
PR 04-AUG-1999: 990S-0147302.
PR 05-AUG-1999: 990S-0147192.
PR 05-AUG-1999: 990S-0147260.
PR 06-AUG-1999: 990S-0147303.
PR 06-AUG-1999: 990S-0147416.
PR 09-AUG-1999: 990S-0147493.
PR 09-AUG-1999: 990S-0147935.
PR 10-AUG-1999: 990S-0148171.
PR 11-AUG-1999: 990S-0148319.
PR 12-AUG-1999: 990S-0148341.
PR 13-AUG-1999: 990S-0148565.
PR 13-AUG-1999: 990S-0148684.
PR 16-AUG-1999: 990S-0149368.
PR 17-AUG-1999: 990S-0149375.
PR 18-AUG-1999: 990S-0149426.
PR 20-AUG-1999: 990S-0149722.
PR 20-AUG-1999: 990S-0149723.
PR 20-AUG-1999: 990S-0149929.
PR 23-AUG-1999: 990S-0149902.
PR 23-AUG-1999: 990S-0149930.
PR 25-AUG-1999: 990S-0150566.
PR 26-AUG-1999: 990S-0150884.
PR 27-AUG-1999: 990S-0151065.
PR 27-AUG-1999: 990S-0151066.
PR 27-AUG-1999: 990S-0151080.
PR 30-AUG-1999: 990S-0151303.
PR 31-AUG-1999: 990S-0151348.
PR 01-SEP-1999: 990S-0151930.
PR 07-SEP-1999: 990S-0152363.
PR 10-SEP-1999: 990S-0153070.
PR 13-SEP-1999: 990S-0153758.
PR 15-SEP-1999: 990S-0154018.
PR 16-SEP-1999: 990S-0154038.
PR 20-SEP-1999: 990S-0154779.
PR 22-SEP-1999: 990S-0155139.
PR 23-SEP-1999: 990S-0155486.

```

```

PR 24-SEP-1999: 990S-0155659.
PR 28-SEP-1999: 990S-0156458.
PR 29-SEP-1999: 990S-0156596.
PR 04-OCT-1999: 990S-0157117.
PR 05-OCT-1999: 990S-0157753.
PR 06-OCT-1999: 990S-0157865.
PR 07-OCT-1999: 990S-0158029.
PR 08-OCT-1999: 990S-0158232.
PR 12-OCT-1999: 990S-0158369.
PR 13-OCT-1999: 990S-0158923.
PR 13-OCT-1999: 990S-0159294.
PR 13-OCT-1999: 990S-0159295.
PR 14-OCT-1999: 990S-0159329.
PR 14-OCT-1999: 990S-0159330.
PR 14-OCT-1999: 990S-0159331.
PR 14-OCT-1999: 990S-0159637.
PR 14-OCT-1999: 990S-0159638.
PR 18-OCT-1999: 990S-0159584.
PR 18-OCT-1999: 990S-0160741.
PR 21-OCT-1999: 990S-0160767.
PR 21-OCT-1999: 990S-0160768.
PR 21-OCT-1999: 990S-0160770.
PR 21-OCT-1999: 990S-0160770.
PR 21-OCT-1999: 990S-0160815.
PR 22-OCT-1999: 990S-0160980.
PR 22-OCT-1999: 990S-0160981.
PR 22-OCT-1999: 990S-0160989.
PR 25-OCT-1999: 990S-0161404.
PR 25-OCT-1999: 990S-0161405.
PR 25-OCT-1999: 990S-0161406.
PR 26-OCT-1999: 990S-0161359.
PR 26-OCT-1999: 990S-0161360.
PR 26-OCT-1999: 990S-0161361.
PR 28-OCT-1999: 990S-0161920.
PR 28-OCT-1999: 990S-0161992.
PR 28-OCT-1999: 990S-0161993.
PR 29-OCT-1999: 990S-0162142.

```

Query Match 5.5%; Score 257.5; DH 21; Length 454;

Post Local Similarity 21.9%; Pred. No. 17e-15; Matches 123; Conservative 83; Mismatches 195; Indels 161; Gaps 26;

```

QY 37 KILGRFOILKTIIPRLCQVVDISRGKHERLVVAEHCERLEDLRRKPVASSTVLGI 96
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 kvrrrrikilrtifmphihtgrvelettsdiyvmeyksqclfytyvckrllqdearnf 65

QY 97 APEWIAQIQQYNNKKGIVHRAISPHNILLDRKGHLKIAFGIYHMTAHGIDVDPICVPSY 156
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 66 lqqlsqveychrmvnhvrdlkrpenllldstcolkiadiqlsmwmdqhlktlscgpy 125

QY 157 IAPFVIAQGIKKTIDHMPKKKPIPSGKSIWWSIGITLPEICVGRKILPQSLDISERLKFL 216
   ||||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 126 daepvlsqkly-----agpovdwscgvlllyalgcglpfddcmipnlfkkl 172

QY 217 LTLDGVDDILVLAEMHCDCDIKELPETYIDLNLKCLTFHPSKRPPDELMKKPSEV 276
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 173 -----kqgiyrlpshlsscaralprmltydvprkltlcpeltrqhrwtqth 217

QY 277 SPLVTPPKVASTLSSSTLRKADLILPEHLSQICDINDVLAEKSIPEVYIACIAGDIL 336
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 218 lprylavls-----ppdlvegakkline-----el 240

QY 337 EKEIVNKKELIKSKPPICILINFLFEDGSRFOGCDKSSILD-----DFTVTLISLCOL 388
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 241 vgevvnn-----mgldingylteslrrntqndatvlyll-1 274

QY 389 RNRLEKDWG--EAFFPLEDDQSN-----LPHNSNNELSAATILPLIR 431
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 275 dnrtrvpsgylscsfgettdsgsnpmrtpeagaspvhwlpahvdhyglqatsqpyv--- 331

QY 432 EKDETYQIN-----RIILFLDRILKAYPYKKNOIMKEAHVDIPPMKGIITMAALIG--- 481
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 332 --drkwaqlqshahprelm-nevklal-qelnwccak-----lghymkcrtwrpaldaq 383

```


Search completed: June 26, 2001, 03:02:51
Job time: 5859 sec

```
PR 28-SEP-1999: 990S-0156458.  
PR 29-SEP-1999: 990S-0156596.  
PR 04-OCT-1999: 990S-0157117.  
PR 05-OCT-1999: 990S-0157753.  
PR 06-OCT-1999: 990S-0157865.  
PR 07-OCT-1999: 990S-0158029.  
PR 08-OCT-1999: 990S-0158232.  
PR 12-OCT-1999: 990S-0158369.  
PR 13-OCT-1999: 990S-0159293.  
PR 13-OCT-1999: 990S-0159294.  
PR 13-OCT-1999: 990S-0159295.  
PR 14-OCT-1999: 990S-0159329.  
PR 14-OCT-1999: 990S-0159330.  
PR 14-OCT-1999: 990S-0159331.  
PR 14-OCT-1999: 990S-0159337.  
PR 14-OCT-1999: 990S-0159638.  
PR 18-OCT-1999: 990S-0159584.  
PR 21-OCT-1999: 990S-0160741.  
PR 21-OCT-1999: 990S-0160767.  
PR 21-OCT-1999: 990S-0160768.  
PR 21-OCT-1999: 990S-0160770.  
PR 21-OCT-1999: 990S-0160814.  
PR 21-OCT-1999: 990S-0160815.  
PR 22-OCT-1999: 990S-0160980.  
PR 22-OCT-1999: 990S-0160981.  
PR 22-OCT-1999: 990S-0160989.  
PR 25-OCT-1999: 990S-0161404.  
PR 25-OCT-1999: 990S-0161405.  
PR 25-OCT-1999: 990S-0161406.  
PR 26-OCT-1999: 990S-0161359.  
PR 26-OCT-1999: 990S-0161360.  
PR 26-OCT-1999: 990S-0161361.  
PR 28-OCT-1999: 990S-0161920.  
PR 28-OCT-1999: 990S-0161992.  
PR 28-OCT-1999: 990S-0161993.  
PR 29-OCT-1999: 990S-0162142.
```

Query Match 5.38; Score 250.5; DB 21; Length 437;
Post Local Similarity 2.44; Pred. No. 7.2e-15;
Matches 108; Conservative 69; Mismatches 187; Indels 79; Gaps 14;

```
QY 46 IKILGRFOILKTIHPRLQGVYDTSKGNHERLVVVAENHGRSLEDLREKRPVSGSTVLC 95  
DB 5 IKVGFELKILIRIMPHILIRGVYELPNDIYVMEYKSGELIDYVEKAKIQEDAEARH 64  
QY 96 IAFVRLQGLQVNMKNKGVYHRAISPHNILLDRKHGKILAKPGIYHMTAHCDDVDPPICGYS 155  
DB 65 IYQILISQVEYCHRMIVHFDIKPENVLIDSGQKIVDQISNMHQKILKLSQSPN 124  
QY 156 YLAPEVIAOGIFKTTDHPKSKPLPSGKSDVWSIGILFELCVGRKLEFOSLDS--ER 212  
DB 125 YDAPEV-----SQAQPY--GPDVATWSCGVILYALIGCLPFDGDIENIPNVFCK 170  
QY 213 LKFLITLDCVDDTLIVLAENHGLDIIKELPEYVIDLNLKCLTFHPSKRPDPDELMDKV 272  
DB 171 IK-----TQMYLIPHLISHARDIPRLMVDPLMRLISLTELQHPW 212  
QY 273 FSHVSPATPTTKPASLSSSIRCADLTPPDISOLCKDINN--DYLAERSLFEHYVIMC 330  
DB 213 IINHPLIYLSLPPIDLDQAKLIEEELIGNVNIQIDRHVDSIAARIQDEALVAGH 270  
QY 331 IAGGLEKEELVKKELIRSKPP-----ICLTP--NFLFEKESFQGRD--RSSILDDTT 380  
DB 271 IIDIRNQSVPNDPFGSKFKQISQGFNSTCPYGNITSHVGHFSALYGIKSNVKDDKT 330  
QY 381 VTLSLCQLNRKLKDVGAFAFFLEDDOSNLP-----HSNSNNE 419  
DB 331 WLIGLQSGQSPYDIMEIKAL-----QNLKICWKIKIQLYNIKORVRSIAYKHNHLE 384  
QY 420 ISAATPIPLIHKKDTEYOINRI 442  
DB 385 DECAIIPLVK--LEIQLYKV 404
```

• • •

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 26, 2001, 01:23:31 : Search time 84.37 Seconds

(without alignments)
5889.158 Million cell updates/sec

Title: US-09-707-121-1

Perfect score: 2682

Sequence: 1 atgttccctgaagacgc.....tccatctctcaatatga 2682

Scoring table: IDENTITY MDC
Gapop 10.0 , Gapext 1.0

Searched: 317530 seqs, 9261069 residues

Total number of hits satisfying chosen parameters: 635060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued_Patents_NA :
2: /cgn2_6/prodata/2/ina/5A_COMB.seq :
3: /cgn2_6/prodata/2/ina/5B_COMB.seq :
4: /cgn2_6/prodata/2/ina/6A_COMB.seq :
5: /cgn2_6/prodata/2/ina/6B_COMB.seq :
6: /cgn2_6/prodata/2/ina/backfil01.seq :

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57.2	2.1	7218	1 US-08-232-463-14	Sequence 14, Appl
2	50.6	1.9	1647	4 US-09-101-146-44	Sequence 44, Appl
3	47	1.8	2754	4 US-09-429-322-3	Sequence 3, Appl
4	42.2	1.6	4163	2 US-08-685-576-5	Sequence 5, Appl
5	40.6	1.5	5053	2 US-08-685-576-2	Sequence 2, Appl
6	40.4	1.5	3018	2 US-08-860-150-6	Sequence 6, Appl
7	40.4	1.5	3018	3 US-09-338-132-6	Sequence 6, Appl
8	39.8	1.5	2104	4 US-09-313-930-1	Sequence 1, Appl
9	39.4	1.5	1541	6 5183884-1	Patent No. 5183884
10	39.4	1.5	1542	1 US-07-978-895-1	Sequence 1, Appl
11	39.4	1.5	1542	1 US-08-473-119-1	Sequence 1, Appl
12	39.4	1.5	1542	1 US-08-475-352-1	Sequence 1, Appl
13	38.6	1.4	2500	5 PCT-US95-05008-3	Sequence 3, Appl
14	38.2	1.4	1251	2 US-09-211-930-2	Sequence 2, Appl
15	38.2	1.4	1251	3 US-09-340-993-2	Sequence 2, Appl
16	38.2	1.4	1353	2 US-09-211-930-8	Sequence 8, Appl
17	38.2	1.4	1353	2 US-09-340-993-8	Sequence 8, Appl
18	38.2	1.4	3201	2 US-09-211-930-1	Sequence 1, Appl
19	38.2	1.4	3201	3 US-09-340-993-1	Sequence 1, Appl
20	37.8	1.4	903	2 US-08-874-347-9	Sequence 9, Appl
21	37.8	1.4	903	3 US-09-093-522-9	Sequence 9, Appl
22	37.6	1.4	2747	2 US-08-874-347-1	Sequence 1, Appl
23	37.6	1.4	2747	3 US-09-093-522-1	Sequence 1, Appl
24	37	1.4	2268	1 US-08-444-005-14	Sequence 14, Appl
25	37	1.4	3312	4 US-09-060-410-1	Sequence 1, Appl
26	37	1.4	4545	6 5183884-3	Patent No. 5183884
27	37	1.4	4905	1 US-07-978-895-3	Sequence 3, Appl

28	37	1.4	4905	1 US-08-473-119-3	Sequence 3, Appl
29	37	1.4	4905	2 US-08-475-352-3	Sequence 3, Appl
30	36.4	1.4	1448	2 US-08-942-218A-1	Sequence 1, Appl
31	36.4	1.4	1881	1 US-08-610-731A-1	Sequence 1, Appl
32	36.4	1.4	1881	2 US-09-067-379-1	Sequence 1, Appl
33	36.4	1.4	1881	3 US-09-067-506-1	Sequence 1, Appl
34	36.4	1.4	2244	4 US-09-094-714A-48	Sequence 48, Appl
35	36.2	1.3	1544	4 US-08-837-593-1	Sequence 1, Appl
36	35.8	1.3	1424	4 US-08-403-634-3	Sequence 3, Appl
37	35.8	1.3	1424	4 US-08-913-441B-3	Sequence 3, Appl
38	35.8	1.3	2434	2 US-08-540-804-15	Sequence 15, Appl
39	35.8	1.3	2434	2 US-08-218-265-15	Sequence 15, Appl
40	35.8	1.3	2434	3 US-08-521-872-15	Sequence 15, Appl
41	35.8	1.3	2434	4 US-08-590-399-15	Sequence 15, Appl
42	35.8	1.3	4739	3 US-08-685-871-1	Sequence 1, Appl
43	35.6	1.3	2248	1 US-08-369-780-1	Sequence 1, Appl
44	35.6	1.3	2248	1 US-08-475-682-1	Sequence 1, Appl
45	35.6	1.3	2248	1 US-08-780-833-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-232-463-14
? Sequence 14, Application US/08232463
? Patent No. 5670367
? GENERAL INFORMATION:
? APPLICANT: DORNER, F.
? APPLICANT: SCHEIFLINGER, F.
? APPLICANT: FALKNER, F. G.
? TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
? NUMBER OF SEQUENCES: 52
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Foley & Lardner
? STREET: 1800 Diagonal Road, Suite 500
? CITY: Alexandria
? STATE: VA
? COUNTRY: USA
? ZIP: 22313-0299
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentio Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/232,463
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/07/935,313
? FILING DATE:
? APPLICATION NUMBER: EP 91 114 300.6
? FILING DATE: 26-AUG-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: BENT, Stephen A.
? REGISTRATION NUMBER: 29,768
? REFERENCE/DOCKET NUMBER: 30472/114 IMM
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703)836-9300
? TELEFAX: (703)683-6109
? TELEX: 899149
? INFORMATION FOR SEQ ID NO: 14:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 7218 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? CLONE: PTZqpt-Fls
? US-08-232-463-14

Tue Jun 26 08:50:47 2001

us-09-707-121-1.rml

Page 8

fb 499 qptcagpt qacvqat aqacvqat fuaagvqat aqet fuaqqaqet cva llll qatq 558
07 472 qvccv fuaqgaa fuaqqaqaa fuaqqaqaa fuaqqaqaa fuaqqaqaa fuaqqaqaa 518
08 559 qvccv fuaqgaa fuaqqaqaa fuaqqaqaa fuaqqaqaa fuaqqaqaa fuaqqaqaa 605

Search completed: June 26, 2001, 08:02:09
Index time: 5418 Sec